

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/743,823A
Source: IFW/b
Date Processed by STIC: 3/29/06

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 03/29/2006

PATENT APPLICATION: US/09/743,823A

TIME: 10:53:54

Input Set : A:\09743823.txt

Output Set: N:\CRF4\03292006\I743823A.raw

3 <110> APPLICANT: Corrado FOGHER
 5 <120> TITLE OF INVENTION: SYNTHETIC POLYNUCLEOTIDE CODING FOR HUMAN LACTOFERRIN,
 VECTORS,
 6 CELLS AND TRANSGENIC PLANTS CONTAINING IT
 8 <130> FILE REFERENCE: 4161-14 / X89727RVP
 10 <140> CURRENT APPLICATION NUMBER: 09/743,823A
 11 <141> CURRENT FILING DATE: 2001-08-22
 13 <150> PRIOR APPLICATION NUMBER: PCT/IT99/00226
 14 <151> PRIOR FILING DATE: 1999-07-19
 16 <150> PRIOR APPLICATION NUMBER: IT RM98A000478
 17 <151> PRIOR FILING DATE: 1998-07-17
 19 <160> NUMBER OF SEQ ID NOS: 26
 21 <170> SOFTWARE: MS Word
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 2079
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial Sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic human
 lactoferrin
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(2076)
 35 <400> SEQUENCE: 1
 36 ggc cgt agg aga agg agt gtt caa tgg tgc gca gta tca caa cca gag 48
 37 Gly Arg Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser Gln Pro Glu
 38 1 5 10 15
 40 gcc aca aaa tgc ttc caa tgg caa agg aat atg aga aaa gtt cgt gga 96
 41 Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val Arg Gly
 42 20 25 30
 44 cct cct gta tct tgc ata aag aga gat tca ccc atc cag tgt atc cag 144
 45 Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys Ile Gln
 46 35 40 45
 48 gca att gcg gaa aac aga gct gat gct gtg act ctt gat ggt ggt ttc 192
 49 Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly Gly Phe
 50 50 55 60
 52 ata tac gag gca gga ctt gcc cca tac aaa ctg cga cct gta gcg gcg 240
 53 Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val Ala Ala
 54 65 70 75 80
 56 gaa gtc tac ggg acc gaa aga caa cca cga act cac tat tat gct gtg 288
 57 Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr Ala Val
 58 85 90 95
 60 gct gtt gtg aag aag ggc gga tct ttt cag ctg aac gaa ctt caa ggt 336
 61 Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu Gln Gly

62

100

105

110

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```

64 ctg aag tca tgc cac aca gga ctt cgc agg acc gct gga tgg aat gtc 384
65 Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp Asn Val
66      115      120      125
68 cct ata ggg aca ctt cgt cca ttc ttg aat tgg acg ggt cca cct gag 432
69 Pro Ile Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro Pro Glu
70      130      135      140
72 ccc att gag gca gct gtg gca aga ttc ttc tca gcc tct tgt gtt cca 480
73 Pro Ile Glu Ala Ala Val Ala Arg Phe Phe Ser Ala Ser Cys Val Pro
74 145      150      155      160
76 ggt gca gat aaa gga caa ttc ccc aac ctt tgt cgc ctg tgt gcg ggg 528
77 Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala Gly
78      165      170      175
80 aca ggg gaa aac aaa tgt gca ttc tca tcc cag gaa ccg tac ttc agc 576
81 Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe Ser
82      180      185      190
84 tac tct ggt gcc ttt aag tgt ctt aga gac ggt gct gga gat gtt gct 624
85 Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val Ala
86      195      200      205
88 ttt att aga gag agc aca gtg ttt gag gat ctt tca gac gag gct gaa 672
89 Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala Glu
90      210      215      220
92 agg gac gag tat gag tta ctc tgc cca gac aac act cgt aag cca gtt 720
93 Arg Asp Glu Tyr Glu Leu Leu Cys Pro Asp Asn Thr Arg Lys Pro Val
94 225      230      235      240
96 gac aag ttc aaa gat tgc cat ctt gca cgg gtc cct tct cat gcc gtt 768
97 Asp Lys Phe Lys Asp Cys His Leu Ala Arg Val Pro Ser His Ala Val
98      245      250      255
100 gtg gca cga agt gtt aat gga aag gag gat gcc atc tgg aat ctt ctc 816
101 Val Ala Arg Ser Val Asn Gly Lys Glu Asp Ala Ile Trp Asn Leu Leu
102      260      265      270
104 cgc caa gca cag gaa aag ttt gga aag gac aag tca ccg aaa ttc cag 864
105 Arg Gln Ala Gln Glu Lys Phe Gly Lys Asp Lys Ser Pro Lys Phe Gln
106      275      280      285
108 ctc ttt ggt tcc cct agt ggg cag aaa gat ctt ctg ttc aag gac tct 912
109 Leu Phe Gly Ser Pro Ser Gly Gln Lys Asp Leu Leu Phe Lys Asp Ser
110      290      295      300
112 gcc att ggg ttt tcg aga gtg cca cct agg ata gat tct ggg ttg tac 960
113 Ala Ile Gly Phe Ser Arg Val Pro Pro Arg Ile Asp Ser Gly Leu Tyr
114 305      310      315      320
116 ctt ggc tcc gga tac ttt act gca att cag aac ttg agg aaa agt gag 1008
117 Leu Gly Ser Gly Tyr Phe Thr Ala Ile Gln Asn Leu Arg Lys Ser Glu
118      325      330      335
120 gag gaa gtt gct gcc cgg cgt gcg cgg gtc gtt tgg tgt gcg gtg gga 1056
121 Glu Glu Val Ala Ala Arg Arg Ala Arg Val Val Trp Cys Ala Val Gly
122      340      345      350
124 gag caa gag ttg cgc aag tgt aac cag tgg agt ggt ttg agc gaa gga 1104
125 Glu Gln Glu Leu Arg Lys Cys Asn Gln Trp Ser Gly Leu Ser Glu Gly
126      355      360      365
128 tct gtg acc tgc tca tcg gcc tcc act aca gaa gat tgc atc gcc ctg 1152

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129 Ser Val Thr Cys Ser Ser Ala Ser Thr Thr Glu Asp Cys Ile Ala Leu
130      370      375      380
132 gtg ttg aaa gga gaa gct gat gcc atg agt ttg gat gga gga tat gtt 1200
133 Val Leu Lys Gly Glu Ala Asp Ala Met Ser Leu Asp Gly Gly Tyr Val
134 385      390      395      400
136 tac act gca ggt aaa tgt ggt ttg gtg cct gtc ctt gca gag aac tac 1248
137 Tyr Thr Ala Gly Lys Cys Gly Leu Val Pro Val Leu Ala Glu Asn Tyr
138      405      410      415
140 aaa tca caa caa agc agt gac cct gat cct aac tgt gtg gat aga cct 1296
141 Lys Ser Gln Gln Ser Ser Asp Pro Asp Pro Asn Cys Val Asp Arg Pro
142      420      425      430
144 gtg gaa gga tat ctt gct gtg gcg gtg gtt agg aga tca gac act agc 1344
145 Val Glu Gly Tyr Leu Ala Val Ala Val Val Arg Arg Ser Asp Thr Ser
146      435      440      445
148 ctt acc tgg aac tct gtg aaa ggc aag aag tcc tgc cac acc gcc gtg 1392
149 Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala Val
150      450      455      460
152 gac agg act gca ggt tgg aat atc ccc atg gga ttg ctc ttc aac cag 1440
153 Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn Gln
154 465      470      475      480
156 acg ggc tcc tgc aaa ttt gat gaa tat ttc agt caa agc tgt gcc cct 1488
157 Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala Pro
158      485      490      495
160 ggt tct gac cca aga tct aat ctc tgt gct ttg tgt att gga gat gag 1536
161 Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp Glu
162      500      505      510
164 caa ggt gag aat aag tgc gtt ccc aac agc aac gag aga tac tac ggt 1584
165 Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr Gly
166      515      520      525
168 tac act ggg gct ttc cgt tgc ttg gct gag aat gct gga gac gtt gca 1632
169 Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val Ala
170      530      535      540
172 ttt gtg aaa gat gtc act gtc ttg cag aac act gat gga aat aac aat 1680
173 Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn Asn
174 545      550      555      560
176 gag gca tgg gct aag gat ttg aag ctt gca gac ttt gcg ttg ctg tgc 1728
177 Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu Cys
178      565      570      575
180 ctc gat ggc aaa cgt aag cct gtg act gaa gct aga agc tgc cat ctt 1776
181 Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His Leu
182      580      585      590
184 gcc atg gcc ccg aat cat gct gtg gtg tct cgt atg gat aag gtg gaa 1824
185 Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val Glu
186      595      600      605
188 cgc ttg aaa cag gtg ttg ctc cac caa cag gct aaa ttt ggt aga aat 1872
189 Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg Asn
190      610      615      620
192 gga tct gac tgc ccg gac aag ttt tgc tta ttc cag tct gaa acc aaa 1920
193 Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr Lys

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194 625          630          635          640
196 aac ctt ttg ttc aat gac aac act gag tgt ctt gcc aga ctc cat ggc 1968
197 Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His Gly
198          645          650          655
200 aaa aca aca tat gaa aaa tat ttg gga cca cag tat gtc gca ggc att 2016
201 Lys Thr Thr Tyr Glu Lys Tyr Leu Gly Pro Gln Tyr Val Ala Gly Ile
202          660          665          670
204 act aat ctg aaa aag tgc tca acc tcc cca ctc cta gaa gcc tgt gaa 2064
205 Thr Asn Leu Lys Lys Cys Ser Thr Ser Pro Leu Leu Glu Ala Cys Glu
206          675          680          685
208 ttc cta agg aag taa 2079
209 Phe Leu Arg Lys
210 690
213 <210> SEQ ID NO: 2
214 <211> LENGTH: 30
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
221 <400> SEQUENCE: 2
222 ggatccatgg gccgtaggag aaggagtgtt 30
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 32
227 <212> TYPE: DNA
228 <213> ORGANISM: Artificial Sequence
230 <220> FEATURE:
231 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
233 <400> SEQUENCE: 3
234 gagctccttc ggttttactt cctgaggaat tc 32
237 <210> SEQ ID NO: 4
238 <211> LENGTH: 42
239 <212> TYPE: DNA
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
245 <400> SEQUENCE: 4
246 tctagataaa ataatctata cattaaaaaa tttgatttta aa 42
249 <210> SEQ ID NO: 5
250 <211> LENGTH: 36
251 <212> TYPE: DNA
252 <213> ORGANISM: Artificial Sequence
254 <220> FEATURE:
255 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
257 <400> SEQUENCE: 5
258 ggatccgact gagtcggata agaagaaaag aaaaga 36
261 <210> SEQ ID NO: 6
262 <211> LENGTH: 36
263 <212> TYPE: DNA
264 <213> ORGANISM: Artificial Sequence

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266 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
269 <400> SEQUENCE: 6
270 tctagagttt tcaaatttga attttaatgt gtgttg 36
273 <210> SEQ ID NO: 7
274 <211> LENGTH: 36
275 <212> TYPE: DNA
276 <213> ORGANISM: Artificial Sequence
278 <220> FEATURE:
279 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
281 <400> SEQUENCE: 7
282 ggatccacc ttaaggaggt tgcaacgagc gtggca 36
285 <210> SEQ ID NO: 8
286 <211> LENGTH: 250
287 <212> TYPE: DNA
288 <213> ORGANISM: Artificial Sequence
290 <220> FEATURE:
291 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
293 <400> SEQUENCE: 8
294 ggccgtagga gaaggagtgt tcaatggtgc gcagtatcac aaccagaggc caaaaaatgc 60
295 ttccaatggc aaaggaatat gagaaaagtt cgtggacctc ctgtatcttg cataaagaga 120
296 gattcaccca tccagtgtat ccaggcaatt gcggaaaaca gagctgatgc tgtgactctt 180
297 gatggtgggt tcatatacga ggcaggactt gcccataca aactgcgacc tgtagcggcg 240
298 gaagtctacg 250
301 <210> SEQ ID NO: 9
302 <211> LENGTH: 250
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
309 <400> SEQUENCE: 9
310 gcacctggaa cacaagaggc tgagaagaat cttgccacag ctgcctcaat gggctcaggt 60
311 ggacccgtcc aattcaagaa tggacgaagt gtccctatag ggacattcca tccagcggtc 120
312 ctgcgaagtc ctgtgtggca tgacttcaga cttgaagtt cgttcagctg aaaagatccg 180
313 cccttcttca caacagccac agcataatag tgagttcgtg gttgtctttc ggtcccgtag 240
314 acttccgcgcg 250
317 <210> SEQ ID NO: 10
318 <211> LENGTH: 250
319 <212> TYPE: DNA
320 <213> ORGANISM: Artificial Sequence
322 <220> FEATURE:
323 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
325 <400> SEQUENCE: 10
326 aactggctta cgagtgttgt ctgggcagag taactcatatc tcgtcccttt cagcctcgtc 60
327 tgaaagatcc tcaaacactg tgctctctct aataaaagca acatctccag caccgtctct 120
328 aagacactta aaggcaccag agtagctgaa gtacggttcc tgggatgaga atgcacattt 180
329 gttttcccct gtccccgcac acaggcgaca aagggtgggg aattgtcctt tatctgcacc 240
330 tggaacacaa 250
333 <210> SEQ ID NO: 11

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:25; N Pos. 534,763,787,789,878

VERIFICATION SUMMARY

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Input Set : A:\09743823.txt

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L:756 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:480

M:341 Repeated in SeqNo=25